

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 23:47:23 ; Search time 3832 Seconds  
(without alignments)  
16974.144 Million cell updates/sec

Title: US-10-055-569A-19  
Perfect score: 1785  
Sequence: 1 atgtcgcgcctgcgactct.....aagggttcattgccttccc 1785

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gsa1: \*  
9: gb\_gsa2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1226.6	68.7	2514	AK049639	Mus muscu
2	1166	65.3	2517	AK010515	Mus muscu
3	1086	61.0	1652	CR615288	full-leng
4	827.8	46.4	1069	EX375153	EX375153
5	741.4	41.5	1006	AL528548	AL528548
6	720	40.3	798	AL529330	AL529330
7	718.6	40.3	883	AL535982	AL535982
8	707.4	39.6	801	BI916059	603184489
9	694.6	38.9	709	CN347351	170004240
10	606.8	34.0	1084	BM559751	AGENCOURT
11	597.4	33.5	599	BI912792	603176235
12	594	33.3	922	CA489555	AGENCOURT
13	588	32.9	772	CA750805	UI-M-PD0-
14	587.2	32.9	709	AL522181	AL522181
15	569.6	31.9	780	BG819418	602781654
16	545.8	30.6	852	EX433210	EX433210
17	523.8	29.3	859	BI522769	603175848
18	512.2	28.7	962	BQ885110	AGENCOURT
19	503.2	28.2	672	BQ613672	UI-M-EMO-
20	493.8	27.7	786	BQ442944	UI-M-EVO-
21	490	27.5	645	CN347350	170006001
22	488	27.3	769	CF731895	UI-M-GZO-
23	476.6	26.7	3282	AK048605	Mus muscu
24	468	26.2	580	CN347356	170005321

25	466	26.1	592	7	CN347348	170005321
26	441.6	24.7	798	5	EX444974	EX444974
27	440.8	24.7	4275	3	BC056941	Mus muscu
28	438.2	24.5	1123	1	AL563186	AL563186
29	430.4	24.1	910	6	CB182208	AGENCOURT
30	398.8	22.3	641	2	BB652629	BB652629
31	395.4	22.2	776	5	BQ884741	AGENCOURT
32	388.4	21.8	390	7	CN347353	170006000
33	383.2	21.5	689	6	CB527206	UI-M-PY0-
34	382.2	21.4	700	6	CB528179	UI-M-FY0-
35	379	21.2	487	6	CD637986	56022172J
36	379	21.2	500	6	CD637985	56022172H
37	379	21.2	506	6	CD637989	56022180H
38	379	21.2	507	6	CD637990	56022180J
39	379	21.2	532	6	CD638023	56022280H
40	379	21.2	537	6	CD638027	56022288H
41	379	21.2	538	6	CD638028	56022288J
42	379	21.2	543	6	CD637980	56021810J
43	378.4	21.2	645	6	BY709932	BY709932
44	375.8	21.1	514	6	CD637993	56022188H
45	375.8	21.1	514	6	CD638032	56022296J

ALIGNMENTS

RESULT 1	AK049639	2514 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	Mus musculus	12 days embryo spinal cord cDNA	RIKEN full-length		
DEFINITION	(CEREBOGLYCAN) (HSPG M13) homolog [Rattus norvegicus], full insert				
ACCESSION	AK049639				
VERSION	AK049639.1	GI:26340377			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipette system				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
REFERENCE	5				

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1785	100.0	1785	6	AX661917	Sequence
2	1777	99.6	2528	6	AX834060	Sequence
3	1777	99.6	2528	9	AX096281	Sequence
4	1777	99.6	2666	9	BC027972	Sequence
5	1775.4	99.5	2509	9	HS085505	Sequence
6	1737.4	97.3	2133	6	AX660027	Sequence
7	1453.4	81.4	1613	6	AX661921	Sequence
8	1231.8	69.0	2607	10	RATCRBLGVC	Sequence
9	1139.4	63.8	1976	6	AX661919	Sequence
10	730.4	40.9	2135	6	AX093588	Sequence
11	358.8	20.1	725	6	AX661923	Sequence
12	340.8	19.1	3515	10	AF105268	Mus musculus
c 13	334.8	18.8	816	6	BD018231	Novel gen
c 14	334.8	18.8	816	6	BD098169	Novel gen
15	332.4	18.6	812	6	BD018230	Novel gen
16	332.4	18.6	812	6	BD098168	Novel gen
17	325.6	18.2	132764	9	AC073842	Human sapi
c 18	325.6	18.2	167854	2	AC092483	Human sapi
19	323	18.1	1677	6	AX937190	Sequence

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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 18:47:40 ; Search time 601 Seconds  
(without alignments)  
15591.043 Million cell updates/sec

Title: US-10-055-569a19  
Perfect score: 1785  
Sequence: 1 atgctcgctgctgacactct.....aagggttcattgcccctttcc 1785

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 4134886 seqs, 2624710521 residues  
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23sep04:\*

- 1: Geneseqn1808s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1785	100.0	1785	6	ABSS1684
2	1785	100.0	1785	10	ADD49088
3	1777	99.6	2528	11	ADM02499
4	1737.4	97.3	2133	6	ABST8649
5	1731	97.0	1762	10	ADD49106
6	1730.6	97.0	1776	10	ADD49086
7	1730.6	97.0	1776	10	ADD49098
8	1621.4	90.8	1648	10	ADD49090
9	1575.6	88.3	1590	10	ADD49104
10	1453.4	81.4	1613	6	ABSS1686
11	1453.4	81.4	1613	10	ADD49092
12	1139.4	63.8	1976	6	ABSS1685
13	1139.4	63.8	1976	10	ADD49100
14	1124.6	63.0	1297	10	ADD49094
15	1101.2	61.7	1126	10	ADD49096
16	783.4	43.9	1283	10	ABST59274
17	732	41.0	1197	8	ABX71193
18	730.4	40.9	2172	6	ABV72861
19	485.4	27.2	495	10	ABST59273
20	373.8	20.9	446	3	Aah30728
21	358.8	20.1	725	6	ABSS1687

22	358.8	20.1	725	10	ADD49102
23	340.8	19.1	1668	12	ADO07731
24	334.8	18.8	816	4	AAI94394
25	332.4	18.6	812	4	AAI94393
26	326	18.3	700	4	AAO08307
27	326	18.3	1624	4	AAO08284
28	323	18.1	1677	8	AAJ54707
29	323	18.1	1677	10	ADP53593
30	323	18.1	1677	12	ADO07726
31	323	18.1	3692	2	AAZ00685
32	323	18.1	3692	8	ABX76377
33	323	18.1	3692	10	ABZ59272
34	323	18.1	3692	10	ACC72657
35	323	18.1	3692	11	ADN39701
36	323	18.1	3692	11	ADN38929
37	323	18.1	3692	12	ADQ19916
38	318.2	17.8	1799	10	ABZ59283
39	318.2	17.8	2579	2	AAZ33983
40	318.2	17.8	2579	3	AAC78482
41	318.2	17.8	2579	4	AAJ45972
42	318.2	17.8	2579	8	ACA63551
43	318.2	17.8	2579	8	ACA89422
44	318.2	17.8	2579	8	ACA73432
45	318.2	17.8	2579	8	ACA05747

ALIGNMENTS

RESULT 1  
ABSS1684

ID ABSS1684 standard; DNA; 1785 BP.

XX AC ABSS1684;

XX DT 05-NOV-2002 (first entry)

XX DE DNA encoding human Glypican-2 Precursor-like protein #1.

XX KW Human; NOVX; pathological condition; NOVX-associated disorder;  
KW Von Hippel-Lindau syndrome; cirrhosis; diabetes; autoimmune disease; infertility;  
KW pancreatitis; obesity; diabetes; glomerulonephritis; glomerulonephritis;  
KW renal artery stenosis; interstitial nephritis; glomerulonephritis;  
KW polycystic kidney disease; cataract; Alzheimer's disease; cancer;  
KW acoustic trauma; cardiomyopathy; atherosclerosis; hypertension;  
KW congenital heart defect; scleroderma; endometriosis; haemophilia;  
KW dementia; stroke; Parkinson's disease; Huntington's disease; epilepsy;  
KW multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis;  
KW acne; wound; asthma; human disease; calpain; epain; zinc finger;  
KW low density lipoprotein B; LDLs; purinocceptor; CG841; synaptotagmin;  
KW serine protease TUSP; mitogen activated protein kinase kinase-2;  
KW Glypican-2 precursor; thymosin beta-10; gene; ds.

XX OS Homo sapiens.

XX XX WO200255702=A2.

XX PD 18-JUL-2002.

XX XX 26-OCT-2001; 2001WO-US050925.

XX PR 26-OCT-2000; 2000US-0243320P.

XX PR 26-OCT-2000; 2000US-0243592P.

XX PR 26-OCT-2000; 2000US-0243642P.

XX PR 27-OCT-2000; 2000US-0243681P.

XX PR 27-OCT-2000; 2000US-0243863P.

XX PR 31-OCT-2000; 2000US-0244433P.

XX PR 01-NOV-2000; 2000US-0244995P.

XX PR 01-NOV-2000; 2000US-0245029P.

XX PR 02-NOV-2000; 2000US-0245293P.

XX PR 02-NOV-2000; 2000US-0245315P.

XX PR 02-NOV-2000; 2000US-0245316P.

XX PR 19-JAN-2001; 2001US-0262994P.